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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/737,319DATE: 07/30/98
TIME: 15:36:29

INPUT SET: S27800.raw

Mayhew

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: KAJIWARA, Susumu
6 MISAWA, Norihiko
7 KONDO, Keiji
8
9 (ii) TITLE OF INVENTION: A DNA CHAIN USEFUL FOR INCREASING
10 PRODUCTION OF CAROTENOIDS
11
12 (iii) NUMBER OF SEQUENCES: 8
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: FOLEY & LARDNER
16 (B) STREET: 3000 K Street, N.W.
17 (C) CITY: Washington
18 (D) STATE: D.C.
19 (E) COUNTRY: U.S.A.
20 (F) ZIP: 20007-5109
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US 08/737,319
30 (B) FILING DATE: 12-NOV-1996
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: PCT/JP96/00574
35 (B) FILING DATE: 08-MAR-1996
36
37 (viii) PRIOR APPLICATION DATA:
38 (A) APPLICATION NUMBER: JP 51234/1995
39 (B) FILING DATE: 10-MAR-1995
40
41 (ix) ATTORNEY/AGENT INFORMATION:
42 (A) NAME: Bent, Stephen A.
43 (B) REGISTRATION NUMBER: 29,768
44 (C) REFERENCE/DOCKET NUMBER: 081356/0111
45
46 (x) TELECOMMUNICATION INFORMATION:

INPUT SET: S27800.raw

47 (A) TELEPHONE: (202) 672-5300
48 (B) TELEFAX: (202) 672-5399
49

50
51 (2) INFORMATION FOR SEQ ID NO:1:
52

53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 251 amino acids
55 (B) TYPE: amino acid
56 (D) TOPOLOGY: linear
57

58 (ii) MOLECULE TYPE: protein
59

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61

62 Met Ser Met Pro Asn Ile Val Pro Pro Ala Glu Val Arg Thr Glu Gly
63 1 5 10 15

64 Leu Ser Leu Glu Glu Tyr Asp Glu Glu Gln Val Arg Leu Met Glu Glu
65 20 25 30

66 Arg Cys Ile Leu Val Asn Pro Asp Asp Val Ala Tyr Gly Glu Ala Ser
67 35 40 45

68 Lys Lys Thr Cys His Leu Met Ser Asn Ile Asn Ala Pro Lys Asp Leu
69 50 55 60

70 Leu His Arg Ala Phe Ser Val Phe Leu Phe Arg Pro Ser Asp Gly Ala
71 65 70 75 80

72 Leu Leu Leu Gln Arg Arg Ala Asp Glu Lys Ile Thr Phe Pro Gly Met
73 85 90 95

74 Trp Thr Asn Thr Cys Cys Ser His Pro Leu Ser Ile Lys Gly Glu Val
75 100 105 110

76 Glu Glu Glu Asn Gln Ile Gly Val Arg Arg Ala Ala Ser Arg Lys Leu
77 115 120 125

78 Glu His Glu Leu Gly Val Pro Thr Ser Ser Thr Pro Pro Asp Ser Phe
79 130 135 140

80 Thr Tyr Leu Thr Arg Ile His Tyr Leu Ala Pro Ser Asp Gly Leu Trp
81 145 150 155 160

82 Gly Glu His Glu Ile Asp Tyr Ile Leu Phe Ser Thr Thr Pro Thr Glu
83 165 170 175

84 His Thr Gly Asn Pro Asn Glu Val Ser Asp Thr Arg Tyr Val Thr Lys
85 180 185 190

86 Pro Glu Leu Gln Ala Met Phe Glu Asp Glu Ser Asn Ser Phe Thr Pro
87 195 200 205

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100
101 Trp Phe Lys Leu Ile Ala Arg Asp Phe Leu Phe Gly Trp Trp Asp Gln
102 210 215 220
103
104 Leu Leu Ala Arg Arg Asn Glu Lys Gly Glu Val Asp Ala Lys Ser Leu
105 225 230 235 240
106
107 Glu Asp Leu Ser Asp Asn Lys Val Trp Lys Met
108 245 250
109
110
111
112 (2) INFORMATION FOR SEQ ID NO:2:
113
114 (i) SEQUENCE CHARACTERISTICS:
115 (A) LENGTH: 259 amino acids
116 (B) TYPE: amino acid
117 (D) TOPOLOGY: linear
118
119 (ii) MOLECULE TYPE: protein
120
121 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
122
123 Met Gln Leu Leu Ala Glu Asp Arg Thr Asp His Met Arg Gly Ala Ser
124 1 5 10 15
125
126 Thr Trp Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys Asp Glu
127 20 25 30
128
129 Cys Ile Leu Val Asp Ala Asp Asp Asn Ile Thr Gly His Val Ser Lys
130 35 40 45
131
132 Leu Glu Cys His Lys Phe Leu Pro His Gln Pro Ala Gly Leu Leu His
133 50 55 60
134
135 Arg Ala Phe Ser Val Phe Leu Phe Asp Asp Gln Gly Arg Leu Leu Leu
136 65 70 75 80
137
138 Gln Gln Arg Ala Arg Ser Lys Ile Thr Phe Pro Ser Val Trp Thr Asn
139 85 90 95
140
141 Thr Cys Cys Ser His Pro Leu His Gly Gln Thr Pro Asp Glu Val Asp
142 100 105 110
143
144 Gln Leu Ser Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys Ala Ala
145 115 120 125
146
147 Ala Ile Arg Lys Leu Glu His Glu Leu Gly Ile Pro Ala His Gln Leu
148 130 135 140
149
150 Pro Ala Ser Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys Ala Ala
151 145 150 155 160
152

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153 Asp Val Gln Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu His Glu
154 165 170 175
155
156 Met Asp Tyr Ile Leu Phe Ile Arg Ala Asn Val Thr Leu Ala Pro Asn
157 180 185 190
158
159 Pro Asp Glu Val Asp Glu Val Arg Tyr Val Thr Gln Glu Glu Leu Arg
160 195 200 205
161
162 Gln Met Met Gln Pro Asp Asn Gly Leu Gln Trp Ser Pro Trp Phe Arg
163 210 215 220
164
165 Ile Ile Ala Ala Arg Phe Leu Glu Arg Trp Trp Ala Asp Leu Asp Ala
166 225 230 235 240
167
168 Ala Leu Asn Thr Asp Lys His Glu Asp Trp Gly Thr Val His His Ile
169 245 250 255
170
171 Asn Glu Ala
172
173
174
175 (2) INFORMATION FOR SEQ ID NO:3:
176
177 (i) SEQUENCE CHARACTERISTICS:
178 (A) LENGTH: 288 amino acids
179 (B) TYPE: amino acid
180 (D) TOPOLOGY: linear
181
182 (ii) MOLECULE TYPE: protein
183
184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
185
186 Met Thr Ala Asp Asn Asn Ser Met Pro His Gly Ala Val Ser Ser Tyr
187 1 5 10 15
188
189 Ala Lys Leu Val Gln Asn Gln Thr Pro Glu Asp Ile Leu Glu Glu Phe
190 20 25 30
191
192 Pro Glu Ile Ile Pro Leu Gln Gln Arg Pro Asn Thr Arg Ser Ser Glu
193 35 40 45
194
195 Thr Ser Asn Asp Glu Ser Gly Glu Thr Cys Phe Ser Gly His Asp Glu
196 50 55 60
197
198 Glu Gln Ile Lys Leu Met Asn Glu Asn Cys Ile Val Leu Asp Trp Asp
199 65 70 75 80
200
201 Asp Asn Ala Ile Gly Ala Gly Thr Lys Lys Val Cys His Leu Met Glu
202 85 90 95
203
204 Asn Ile Glu Lys Gly Leu Leu His Arg Ala Phe Ser Val Phe Ile Phe
205 100 105 110

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206
207 Asn Glu Gln Gly Glu Leu Leu Leu Gln Gln Arg Ala Thr Glu Lys Ile
208 115 120 125
209
210 Thr Phe Pro Asp Leu Trp Thr Asn Thr Cys Cys Ser His Pro Leu Cys
211 130 135 140
212
213 Ile Asp Asp Glu Leu Gly Leu Lys Gly Lys Leu Asp Asp Lys Ile Lys
214 145 150 155 160
215
216 Gly Ala Ile Thr Ala Ala Val Arg Lys Leu Asp His Glu Leu Gly Ile
217 165 170 175
218
219 Pro Glu Asp Glu Thr Lys Thr Arg Gly Lys Phe His Phe Leu Asn Arg
220 180 185 190
221
222 Ile His Tyr Met Ala Pro Ser Asn Glu Pro Trp Gly Glu His Glu Ile
223 195 200 205
224
225 Asp Tyr Ile Leu Phe Tyr Lys Ile Asn Ala Lys Glu Asn Leu Thr Val
226 210 215 220
227
228 Asn Pro Asn Val Asn Glu Val Arg Asp Phe Lys Trp Val Ser Pro Asn
229 225 230 235 240
230
231 Asp Leu Lys Thr Met Phe Ala Asp Pro Ser Tyr Lys Phe Thr Pro Trp
232 245 250 255
233
234 Phe Lys Ile Ile Cys Glu Asn Tyr Leu Phe Asn Trp Trp Glu Gln Leu
235 260 265 270
236
237 Asp Asp Leu Ser Glu Val Glu Asn Asp Arg Gln Ile His Arg Met Leu
238 275 280 285
239
240
241
242 (2) INFORMATION FOR SEQ ID NO:4:
243
244 (i) SEQUENCE CHARACTERISTICS:
245 (A) LENGTH: 1099 base pairs
246 (B) TYPE: nucleic acid
247 (C) STRANDEDNESS: double
248 (D) TOPOLOGY: linear
249
250 (ii) MOLECULE TYPE: DNA (genomic)
251
252 (ix) FEATURE:
253 (A) NAME/KEY: CDS
254 (B) LOCATION: 99..851
255
256
257
258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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SEQUENCE VERIFICATION REPORT
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Original Text